

BLAST

Basic Local Alignment Search Tool

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Protein Sequence (67 letters)

Results for: ▾

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID lcl|15335
 lcl|15335**Description**

None

Molecule type

amino acid

Query Length

67

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

ProgramBLASTP 2.2.22+ [Citation](#)**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference - compositional score matrix adjustment

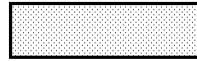
Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#) [\[Distance tree of results\]](#) [\[Related Structures\]](#) [\[Multiple alignment\]](#) NEW

[Search Parameters](#)

Search parameter name Search parameter value

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Filter string	F
Genetic Code	1
Window Size	40



Threshold	11
Composition-based stats	2
Database	

Database parameter name Database parameter value

Posted date	Feb 16, 2010 5:41 PM
Number of letters	3,560,334,713
Number of sequences	10,435,126
Entrez query	none

Karlin-Altschul statistics

Params Ungapped Gapped

Lambda	0.315511	0.267
K	0.129695	0.041
H	0.4138	0.14

Results Statistics

Results Statistics parameter name Results Statistics parameter value

Length adjustment	39
Effective length of query	28
Effective length of database	3153364799
Effective search space	88294214372
Effective search space used	88294214372

[Graphic Summary](#)

[Show Conserved Domains](#)

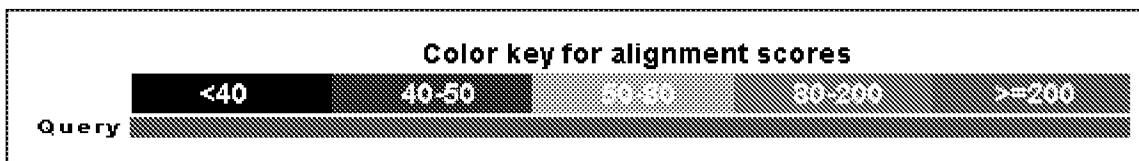
No putative conserved domains have been detected

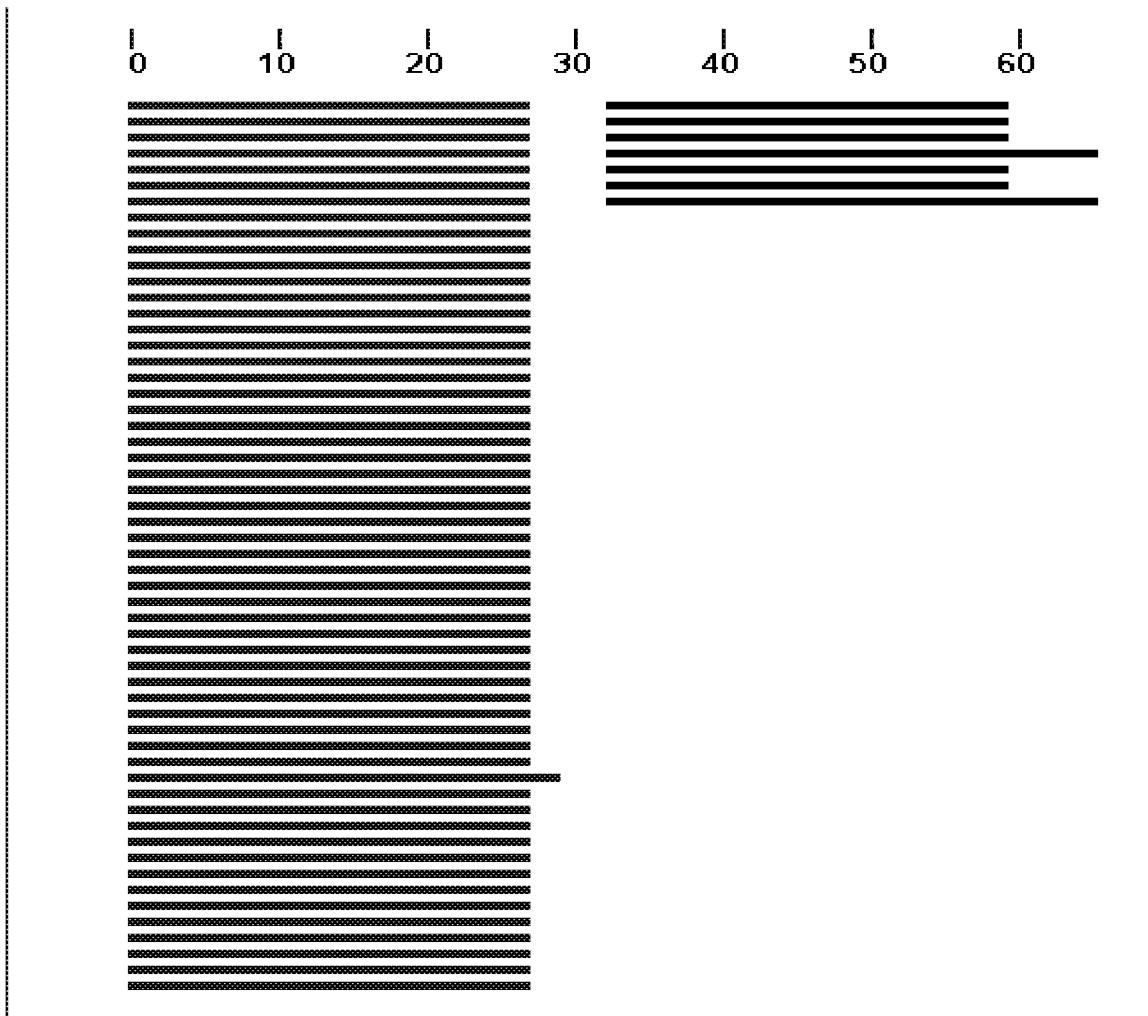


Distribution of 100 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





Descriptions

E	Score
Sequences producing significant alignments:	(Bits) Value
gb AAB25018.1 PR1(Fv)-PE38KDEL heavy and light chain variabl...	45.1 0.002
gb AAD09194.1 anti-asialo GM1 ganglioside antibody heavy cha...	45.1 0.003
pir A2S912 Ig heavy chain precursor V region (W3129) - mouse...	44.7 0.003
spi P01807.1 HVM37_MOUSE RecName: Full=Ig heavy chain V region...	44.7 0.003
prf 1005282A Ig M V-H	44.7 0.003
gb AAH96617.1 Ig protein [Mus musculus]	44.7 0.003
spi P01806.1 HVM36_MOUSE RecName: Full=Ig heavy chain V region...	44.7 0.003
spi P01808.1 HVM38_MOUSE RecName: Full=Ig heavy chain V region...	44.7 0.003
pir A47329 Ig heavy chain V region (PR1) - mouse	44.7 0.004
gb AAA20135.1 immunoglobulin heavy chain [Mus musculus]	44.3 0.004
gb AAT06081.1 immunoglobulin heavy chain variable region [Mu...	44.3 0.004
gb AAA38079.1 Ig heavy chain VH-D-JH4 region [Mus musculus]	44.3 0.004
gb ABO26565.1 anti-rabies glycoprotein immunoglobulin heavy ...	44.3 0.004
gb AAQ73025.1 anti-meningococcal polysaccharide group C mono...	44.3 0.004
gb ABR89741.1 immunoglobulin heavy chain variable region [Mu...	44.3 0.004
gb AAQ74725.1 immunoglobulin mu heavy chain variable region ...	44.3 0.004
prf 1005282D Ig M V-H	44.3 0.004
gb AAT81547.1 immunoglobulin gamma 2b heavy chain variable r...	44.3 0.004
gb AAM12009.1 monoclonal anti-alpha-1,3-galactosyltransferas...	44.3 0.004
gb AAQ74712.1 immunoglobulin mu heavy chain variable region ...	44.3 0.005
gb AAO19662.1 immunoglobulin heavy chain variable region [Mu...	44.3 0.005
dbj BAA74965.1 natural polyreactive IgA antibody [Mus musculus]	44.3 0.005
gb AAK68991.1 AF222891.1 monoclonal anti-alpha-1,3-galactosyl...	44.3 0.005
pir I67528 CD33 antigen homolog - mouse (fragment) >gb AAP19...	44.3 0.005
gb AAT81549.1 immunoglobulin gamma 1 heavy chain variable re...	43.9 0.005
gb AAO13541.1 immunoglobulin heavy chain variable region [Mu...	43.9 0.005
gb AAA38621.1 Ig heavy chain V-region [Mus musculus]	43.9 0.005
gb AAC60709.1 Shigella dysenteriae type 1-specific antibody ...	43.9 0.005
gb AAQ74729.1 immunoglobulin mu heavy chain variable region ...	43.9 0.005
gb AAA38619.1 Ig heavy chain V-region [Mus musculus]	43.9 0.006
gb ACI42269.1 immunoglobulin heavy chain variable region [Mu...	43.9 0.006
gb ACI42266.1 immunoglobulin heavy chain variable region [Mu...	43.5 0.007
gb ACI42252.1 immunoglobulin heavy chain variable region [Mu...	43.5 0.007
emb CAA05027.1 variable region of IgE heavy chain [Mus muscu...	42.7 0.013
pir S13791 Ig heavy chain V region (X-24) - mouse	42.4 0.014
prf 1005282C Ig M V-H	42.4 0.014
gb AAA38620.1 Ig heavy chain V-region [Mus musculus]	42.4 0.015
pdb 1YOL H Chain H, Catalytic Elimination Antibody 34e4 In Co...	42.4 0.015
pdb 3CFJ H Chain H, Crystal Structure Of Catalytic Eliminatio...	42.4 0.016
gb EDL37189.1 mCG55588 [Mus musculus]	42.4 0.016
gb AAA37971.1 Ig H-chain V-D-region [Mus musculus]	42.4 0.016
spi P01809.1 HVM39_MOUSE RecName: Full=Ig heavy chain V region...	42.4 0.016
gb AAA38338.1 Ig mu chain V-region [Mus musculus]	42.4 0.017
gb AAA38335.1 immunoglobulin heavy chain VJ region [Mus musc...	42.4 0.018
gb AAO19012.1 immunoglobulin heavy chain variable region [Mu...	42.0 0.019
pdb 1UZ8 B Chain B, Anti-Lewis X Fab Fragment In Complex With...	42.0 0.020
pdb 1UZ6 F Chain F, Anti-Lewis X Fab Fragment Uncomplexed >pd...	42.0 0.020
emb CAA25678.1 unnamed protein product [Mus musculus]	42.0 0.021
pir I67527 CD33 antigen homolog - mouse (fragment) >gb AAP20...	42.0 0.022
emb CAA70114.1 immunoglobulin heavy chain [Mus musculus]	42.0 0.022
dbj BAA88633.1 CN 8 single chain antibody [synthetic construct]	41.2 0.032
prf 17101628 Ig M L	41.2 0.032

gb ABD72270.1	anti-human gastric carcinoma immunoglobulin he...	41.2	0.039
gb AAK69384.1	AF2223151_1 anti-alpha(1,3)Gal monoclonal antibo...	40.8	0.040
gb ABA42888.1	anti-CD-38 immunoglobulin heavy chain variable...	40.8	0.047
sp P01812.1	HVM42_MOUSE RecName: Full=Ig heavy chain V region...	40.8	0.048
gb AAC13298.1	monoclonal antibody ah7:35 IgG1 heavy chain [M...	40.8	0.049
pdb 1Y18 H	Chain H, Fab Fragment Of Catalytic Elimination Ant...	40.8	0.050
dbj BAC28985.1	unnamed protein product [Mus musculus]	40.4	0.054
gb AAA38287.1	immunoglobulin active Ab3 heavy chain variable...	40.4	0.065
gb AAA91994.1	immunoglobulin heavy chain [Mus musculus]	40.4	0.065
gb AAA38290.2	immunoglobulin active Ab3 heavy chain variable...	40.0	0.069
gb AAO59819.1	AF458197_1 immunoglobulin heavy chain VDJ [Mus ...	40.0	0.072
sp P01810.1	HVM40_MOUSE RecName: Full=Ig heavy chain V region...	40.0	0.079
gb ACC59096.1	anti-sulfadimidine immunoglobulin single chain...	39.7	0.094
pdb 2FBJ H	Chain H, Refined Crystal Structure Of The Galactan...	39.7	0.10
gb AAA37953.1	Ig H-chain V-D-region [Mus musculus]	39.7	0.11
pdb 1OTS C	Chain C, Structure Of The Escherichia Coli Clc Chl...	39.3	0.12
gb AAA38080.1	Ig heavy chain VH-D-JH3 region [Mus musculus]	39.3	0.12
ddb 2H2P C	Chain C, Crystal Structure Of Clc-Ec1 In Complex W...	39.3	0.12
gb AAA21376.1	immunoglobulin heavy chain [Mus musculus]	39.3	0.13
prf 11710162A	Ig M H	39.3	0.14
pir 1S06817	Ig heavy chain V region (clone 11C7) - mouse >emb...	39.3	0.15
gb AAA37969.1	Ig H-chain V-D-region [Mus musculus]	38.9	0.16
gb AAA38354.1	immunoglobulin heavy chain VJ region [Mus musc...	38.9	0.17
sp P01811.1	HVM41_MOUSE RecName: Full=Ig heavy chain V region...	38.9	0.19
gb AAA37951.1	Ig H-chain V-D-region [Mus musculus]	38.5	0.20
gb AAA38336.1	Ig mu chain V-region [Mus musculus]	38.1	0.31
gb AAA37970.1	Ig H-chain V-D-region [Mus musculus]	38.1	0.32
pdb 2C10 A	Chain A, Enaiihis Fab Fragment In The Free Form >p...	37.7	0.34
gb AAA37952.1	Ig H-chain V-D-region [Mus musculus]	37.7	0.35
gb AAA38622.1	Ig heavy chain V-region [Mus musculus]	37.7	0.37
gb EDL89039.1	rCG21048 [Rattus norvegicus]	37.4	0.50
gb AAA38286.1	immunoglobulin active Ab3 heavy chain variable...	37.4	0.55
pir 1A30560	Ig heavy chain V region (16.4.12E) - mouse (fragm...	37.4	0.55
gb AAD26785.1	immunoglobulin heavy chain VH11-JH4 region [Mu...	37.0	0.59
pir 1S20709	Ig kappa chain V region - mouse >emb CAA77975.1 ...	37.0	0.70
gb AAB48807.1	anti-DNA immunoglobulin light chain IgG [Mus m...	37.0	0.73
emb CAA46669.1	monoclonal antibody CB-mab-p24 /13-5 VJ regio...	35.8	1.6
emb CAR846114.1	immunoglobulin light chain variable region [M...	35.8	1.6
gb EDK98812.1	mCG1036498 [Mus musculus]	35.4	1.7
gb AAK68992.1	AF2222892_1 monoclonal anti-alpha-1,3-galactosyl...	35.4	1.7
gb AAAS1145.1	Ig kappa chain [Mus musculus]	35.4	1.8
gb EDL83204.1	rCG64160 [Rattus norvegicus]	35.4	1.8
gb AAM16273.1	immunoglobulin kappa light chain variable regi...	35.4	1.9
pir 1C32513	Ig kappa chain precursor V region (BXW14) - mouse...	35.4	2.0
gb EDK98809.1	mCG130744 [Mus musculus]	35.4	2.2
pir 1AJ6259	ig kappa chain V region (TE34) - mouse	35.0	2.2
gb AAP79429.1	anti-potato cyst nematode monoclonal antibody ...	35.0	2.6
gb EDL83206.1	rCG64161 [Rattus norvegicus]	34.7	2.9

Alignments Select All Get selected sequences Distance tree of results Multiple alignment NEW

>**gb|AAB25018.1|** PR1(Fv)-PE38KDEL heavy and light chain variable region [synthetic construct]
Length=243

Score = 45.1 bits (105), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)



Query 1 GFDFRRNWMS-----EINPDSSKINYTPSLKD 27
 GFDF R WMS EINPDSS INYTPSLKD
 Sbjct 27 GFDFSRWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD 67

>**gb|AAD09194.1|** anti-asialo GM1 ganglioside antibody heavy chain variable region [Mus musculus]
 Length=118

Score = 45.1 bits (105), Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

Query 1 GFDFRRNWMS-----EINPDSSKINYTPSLKD 27
 GFDF R WMS EINPDSS INYTPSLKD
 Sbjct 26 GFDFSRWMSWVRQAPGKGLESIPEINPDSSTINYTPSLKD 66

>**pir||A25912** Ig heavy chain precursor V region (W3129) - mouse
gb|AAA38228.1| Ig H-chain precursor (V-J4-C) [Mus musculus]
 Length=139

Score = 44.7 bits (104), Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

Query 1 GFDFRRNWMS-----EINPDSSKINYTPSLKD 27
 GFDF R WMS EINPDSS INYTPSLKD
 Sbjct 44 GFDFSRWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD 84

>**sp|P01807.1|HVM37_MOUSE** RecName: Full=Ig heavy chain V region X44
 Length=119

Score = 44.7 bits (104), Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

Query 1 GFDFRRNWMS-----EINPDSSKINYTPSLKD 27
 GFDF R WMS EINPDSS INYTPSLKD
 Sbjct 26 GFDFSRWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD 66

>**prf||1005282A** Ig M V-H
 Length=119

Score = 44.7 bits (104), Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

Query 1 GFDFRRNWMS-----EINPDSSKINYTPSLKD 27
 GFDF R WMS EINPDSS INYTPSLKD
 Sbjct 26 GFDFSRWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD 66

>**gb|AAH96617.1|** Ig protein [Mus musculus]
 Length=476

Gene ID: 544903 LOC544903 | similar to immunoglobulin mu-chain [Mus musculus]
 (10 or fewer PubMed links)

Score = 44.7 bits (104), Expect = 0.003, Method: Composition-based stats.
 Identities = 22/41 (53%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

Query 1 GFDFRRNWMS-----EINPDSSKINYTPSLKD 27
 GFDF ++WMS EINPDSS INY PSLKD
 Sbjct 44 GFDFSKDWMSWVRQAPGKGLEWIGEINPDSSTINYAPSLKD 84

>**sp|P01806.1|HVM36_MOUSE** RecName: Full=Ig heavy chain V region 441; Flags: Pre
emb|CAA24152.1| immunoglobulin heavy chain [Mus musculus]
 Length=116

Gene ID: 195176 Ig-VX24 | immunoglobulin heavy chain (X24 family)
 [Mus musculus] (Over 10 PubMed links)

Score = 44.7 bits (104), Expect = 0.003, Method: Compositional matrix adjust.



Identities = 24/41 (58%) , Positives = 24/41 (58%) , Gaps = 14/41 (34%)

Query 1	GFDFRWNWMS-----	EINPDSSKINYTPSLKD	27
	GFDF R WMS	EINPDSS INYTPSLKD	
Sbjct 44	GFDFSRWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD		84

>**sp|P01808.1|HVM38_MOUSE** RecName: Full=Ig heavy chain V region T601
Length=119

Score = 44.7 bits (104), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 24/41 (58%) , Positives = 24/41 (58%) , Gaps = 14/41 (34%)

Query 1	GFDFRWNWMS-----	EINPDSSKINYTPSLKD	27
	GFDF R WMS	EINPDSS INYTPSLKD	
Sbjct 26	GFDFSRWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD		66

>**pir|A47329** Ig heavy chain V region (PR1) - mouse
Length=118

Score = 44.7 bits (104), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 24/41 (58%) , Positives = 24/41 (58%) , Gaps = 14/41 (34%)

Query 1	GFDFRWNWMS-----	EINPDSSKINYTPSLKD	27
	GFDF R WMS	EINPDSS INYTPSLKD	
Sbjct 27	GFDFSRWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD		67

>**gb|AAA20135.1| immunoglobulin heavy chain [Mus musculus]**
Length=116

Score = 44.3 bits (103), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 24/41 (58%) , Positives = 24/41 (58%) , Gaps = 14/41 (34%)

Query 1	GFDFRWNWMS-----	EINPDSSKINYTPSLKD	27
	GFDF R WMS	EINPDSS INYTPSLKD	
Sbjct 26	GFDFSRWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD		66

>**gb|AAT06081.1| immunoglobulin heavy chain variable region [Mus musculus]**
Length=122

Score = 44.3 bits (103), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 24/41 (58%) , Positives = 24/41 (58%) , Gaps = 14/41 (34%)

Query 1	GFDFRWNWMS-----	EINPDSSKINYTPSLKD	27
	GFDF R WMS	EINPDSS INYTPSLKD	
Sbjct 26	GFDFSRWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD		66

>**gb|AAA38079.1| Ig heavy chain VH-D-JH4 region [Mus musculus]**
Length=113

Score = 44.3 bits (103), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 24/41 (58%) , Positives = 24/41 (58%) , Gaps = 14/41 (34%)

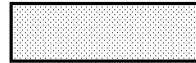
Query 1	GFDFRWNWMS-----	EINPDSSKINYTPSLKD	27
	GFDF R WMS	EINPDSS INYTPSLKD	
Sbjct 22	GFDFSRWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD		62

>**gb|AB026565.1| anti-rabies glycoprotein immunoglobulin heavy chain variable region [synthetic construct]**
Length=125

Score = 44.3 bits (103), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 24/41 (58%) , Positives = 24/41 (58%) , Gaps = 14/41 (34%)

Query 1	GFDFRWNWMS-----	EINPDSSKINYTPSLKD	27
	GFDF R WMS	EINPDSS INYTPSLKD	
Sbjct 25	GFDFSRWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD		65

>**gb|AA073025.1| anti-meningococcal polysaccharide group C monoclonal antibody 2010.10 immunoglobulin heavy chain [Mus musculus]**



Length=118

Score = 44.3 bits (103), Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

Query 1 GFDFRWNWMS-----EINPDSSKINYTPSLKD 27
 GFDF R WMS EINPDSS INYTPSLKD
 Sbjct 26 GFDFSRWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD 66

>gb|ABB89741.1| immunoglobulin heavy chain variable region [Mus musculus]
 Length=115

Score = 44.3 bits (103), Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

Query 1 GFDFRWNWMS-----EINPDSSKINYTPSLKD 27
 GFDF R WMS EINPDSS INYTPSLKD
 Sbjct 26 GFDFSRWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD 66

>gb|AAQ74725.1| immunoglobulin mu heavy chain variable region [Mus musculus]
 Length=110

Score = 44.3 bits (103), Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

Query 1 GFDFRWNWMS-----EINPDSSKINYTPSLKD 27
 GFDF R WMS EINPDSS INYTPSLKD
 Sbjct 18 GFDFSRWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD 58

>prf||1005282D Ig M V-H
 Length=119

Score = 44.3 bits (103), Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

Query 1 GFDFRWNWMS-----EINPDSSKINYTPSLKD 27
 GFDF R WMS EINPDSS INYTPSLKD
 Sbjct 26 GFDFSRWMSWVRQAPGKGPDWIGEINPDSSTINYTPSLKD 66

>gb|AAT81547.1| immunoglobulin gamma 2b heavy chain variable region [Mus musculus]
 >gb|AAT81548.1| immunoglobulin gamma 3 heavy chain variable region [Mus musculus]
 Length=99

Score = 44.3 bits (103), Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

Query 1 GFDFRWNWMS-----EINPDSSKINYTPSLKD 27
 GFDF R WMS EINPDSS INYTPSLKD
 Sbjct 26 GFDFSRWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD 66

>gb|AAM12009.1| monoclonal anti-alpha-1,3-galactosyltransferase IgM heavy chain
 [Mus musculus]
 Length=151

Score = 44.3 bits (103), Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

Query 1 GFDFRWNWMS-----EINPDSSKINYTPSLKD 27
 GFDF R WMS EINPDSS INYTPSLKD
 Sbjct 26 GFDFSRWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD 66

>gb|AAQ74712.1| immunoglobulin mu heavy chain variable region [Mus musculus]
 Length=104

Score = 44.3 bits (103), Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

Query 1 GFDFRWNWMS-----EINPDSSKINYTPSLKD 27
 GFDF R WMS EINPDSS INYTPSLKD
 Sbjct 18 GFDFSRWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD 58